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BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/019,372
Source: O1PG
Date Processed by STIC: 1/2/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>>), EFS Submission

User Manual - ePAVE

2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202

3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

Or

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202

4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <i>10/017, 372</i>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 1 st amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If Intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.	
10 <input checked="" type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/017,372

DATE: 01/02/2002
TIME: 11:25:32

Input Set : A:\61302.ST25.txt
Output Set: N:\CRF3\01022002\J017372.raw

pp 1-3,5
Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Wolfraim, Lawrence
 4 Letterio, John
 6 <120> TITLE OF INVENTION: FUNCTIONALIZED TGF-BETA FUSION PROTEINS
 8 <130> FILE REFERENCE: 4239-61302
 C 10 <140> CURRENT APPLICATION NUMBER: US/10/017,372
 C 10 <141> CURRENT FILING DATE: 2001-10-19
 10 <150> PRIOR APPLICATION NUMBER: 60/242,292
 11 <151> PRIOR FILING DATE: 2000-10-20
 13 <160> NUMBER OF SEQ ID NOS: 39
 15 <170> SOFTWARE: PatentIn version 3.1
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 28
 19 <212> TYPE: DNA
 20 <213> ORGANISM: synthetic oligonucleotide
 22 <400> SEQUENCE: 1
 23 ggagagatct ggtaccgaga tggcgctt 28
 26 <210> SEQ ID NO: 2
 27 <211> LENGTH: 42
 28 <212> TYPE: DNA
 29 <213> ORGANISM: synthetic oligonucleotide
 31 <400> SEQUENCE: 2 42
 32 ataagaatg cggccgctt aatcgatccc aagtgggctt gg
 35 <210> SEQ ID NO: 3
 36 <211> LENGTH: 48
 37 <212> TYPE: DNA
 38 <213> ORGANISM: synthetic oligonucleotide
 40 <400> SEQUENCE: 3
 41 gactacaagg atgacgacga caaggccctg gataccaaact actgcttc 48
 44 <210> SEQ ID NO: 4
 45 <211> LENGTH: 45
 46 <212> TYPE: DNA
 47 <213> ORGANISM: synthetic oligonucleotide
 49 <400> SEQUENCE: 4 45
 50 cttgtcgtcg tcatccttgt agtctcggcg gtgccgggag ctgtg
 53 <210> SEQ ID NO: 5
 54 <211> LENGTH: 45
 55 <212> TYPE: DNA
 56 <213> ORGANISM: synthetic oligonucleotide
 58 <400> SEQUENCE: 5
 59 gactacaagg atgacgacga caggagaaga actgctgcgt gcggc 45
 62 <210> SEQ ID NO: 6
 63 <211> LENGTH: 45
 64 <212> TYPE: DNA
 65 <213> ORGANISM: synthetic oligonucleotide
 67 <400> SEQUENCE: 6
 68 cttgtcgtcg tcatccttgt agtctcggcg gtgccgggag ctgtg 45
 71 <210> SEQ ID NO: 7

see item 10 on Exam Summary Sheet

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/017,372

DATE: 01/02/2002
TIME: 11:25:32

Input Set : A:\61302.ST25.txt
Output Set: N:\CRF3\01022002\J017372.raw

72 <211> LENGTH: 8
 73 <212> TYPE: PRT
 74 <213> ORGANISM: synthetic oligopeptide
 76 <400> SEQUENCE: 7
 78 Asp Tyr Lys Asp Asp Asp Asp Lys
 79 1 5
 82 <210> SEQ ID NO: 8
 83 <211> LENGTH: 1197
 84 <212> TYPE: DNA
 85 <213> ORGANISM: fusion
 87 <220> FEATURE:
 88 <221> NAME/KEY: CDS
 89 <222> LOCATION: (1)..(1197)
 90 <223> OTHER INFORMATION:
 93 <220> FEATURE:
 94 <221> NAME/KEY: misc_feature
 95 <222> LOCATION: (278)..(279)
 96 <223> OTHER INFORMATION: Maturation cleavage site
 99 <400> SEQUENCE: 8 48
 100 atg gcg cct tcg ggg ctg cgg ctc ttg ccg ctg ctg ctg ccg ctg ctg 48
 101 Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Pro Leu Leu
 102 1 5 10 15
 104 tgg ctg cta gtg ctg acc cct ggc cgg ccg gcc gca ctg tcc acc 96
 105 Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
 106 20 25 30
 108 tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc atc gag gcc 144
 109 Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
 110 35 40 45
 112 att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc ccc ccg agc 192
 113 Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
 114 50 55 60
 116 cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta ctg gct ctt 240
 117 Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
 118 65 70 75 80
 120 tac aac agt acc cgc gac cgg gta gcc ggg gaa agt gtc gaa ccg gag 288
 121 Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
 122 85 90 95
 124 ccc gag cca gag gcg gac tac tac gcc aag gag gtc acc cgc gtg cta 336
 125 Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
 126 100 105 110
 128 atg gtg gaa agc ggc aac caa atc tat gat aaa ttc aag ggc acc ccc 384
 129 Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
 130 115 120 125
 132 cac agc tta tat atg ctg ttc aac acg tcg gag ctc cgg gaa gcg gtg 432
 133 His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
 134 130 135 140
 136 ccg gaa cct gta ttg ctc tct cgg gca gag ctg cgc ctg ctg agg ctc 480
 137 Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
 138 145 150 155 160

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/017,372

DATE: 01/02/2002
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Input Set : A:\61302.ST25.txt
Output Set: N:\CRF3\01022002\J017372.raw

140	aag tta aaa gtg gag cag cac gtg gag cta tac cag aaa tac agc aat	528
141	Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn	
142	165 170 175	
144	gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc ccc agt gac tca	576
145	Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser	
146	180 185 190	
148	ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg cgg cag tgg ctg	624
149	Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu	
150	195 200 205	
152	acc cgc aga gag gct ata gag ggt ttt cgc ctc agt gcc cac tct tcc	672
153	Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser	
154	210 215 220	
156	tct gac agc aaa gat aac aca ctc cac gtg gaa att aac ggg ttc aat	720
157	Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn	
158	225 230 235 240	
160	tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc atg aac cgg ccc	768
161	Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro	
162	245 250 255	
164	tcc ctg ctc ctc atg gcc acc cgg ctg gag agg gcc cag cac ctg cac	816
165	Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His	
166	260 265 270	
168	agc tcc cgg cac cgc cga gac tac aag gat gac gac aag gcc ctg	864
169	Ser Ser Arg His Arg Arg Asp Tyr Lys Asp Asp Asp Lys Ala Leu	
170	275 280 285	
172	gat acc aac tac tgc ttc agc tcc acg gag aag aac tgc tgc gtg cgg	912
173	Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg	
174	290 295 300	
176	cag ctc tac att gac ttc cgg aag gac ctg ggc tgg aag tgg att cat	960
177	Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His	
178	305 310 315 320	
180	gaa ccc aag ggc tac cat gcc aat ttc tgc ctg ggg ccc tgt ccc tac	1008
181	Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr	
182	325 330 335	
184	atc tgg agc cta gac act cag tac agc aag gtc ctg gct ctg tac aac	1056
185	Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn	
186	340 345 350	
188	cag cac aac ccg ggc gcg tcg gcg gcg ccg tgc tgc gtg ccg cag gcg	1104
189	Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala	
190	355 360 365	
192	ctg gag cca ctg ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg	1152
193	Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val	
194	370 375 380	
196	gag cag ctg tcc aac atg atc gtg cgt tcc tgc aag tgc agc tga	1197
197	Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser	
198	385 390 395	
201	<210> SEQ ID NO: 9	
202	<211> LENGTH: 398	
203	<212> TYPE: PRT	
204	<213> ORGANISM: fusion	

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/017,372

DATE: 01/02/2002
TIME: 11:25:32

Input Set : A:\61302.ST25.txt
Output Set: N:\CRF3\01022002\J017372.raw

206 <220> FEATURE:
 207 <221> NAME/KEY: misc_feature
 208 <222> LOCATION: (278)..(279)
 209 <223> OTHER INFORMATION: Maturation cleavage site
 211 <400> SEQUENCE: 9
 213 Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Pro Leu Leu
 10 15
 214 1 5 1
 217 Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
 20 25 30
 218 Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
 35 40 45
 222 Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
 50 55 60
 226 Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
 65 70 75 80
 230 Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
 85 90 95
 234 Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
 100 105 110
 238 Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
 115 120 125
 242 His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
 130 135 140
 246 Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
 145 150 155 160
 250 Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
 165 170 175
 253 Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
 180 185 190
 258 Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
 195 200 205
 261 Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
 210 215 220
 266 Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
 225 230 235 240
 273 Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
 245 250 255
 274 Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg
 260 265 270
 278 Ser Ser Arg His Arg Arg Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu
 275 280 285
 282 Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His
 290 295 300
 289 Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
 305 310 315 320
 293 Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
 325 330 335
 297 340 345 350
 298

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/017,372

DATE: 01/02/2002
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Input Set : A:\61302.ST25.txt
Output Set: N:\CRF3\01022002\J017372.raw

301 Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
302 355 360 365
305 Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
306 370 375 380
309 Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
310 385 390 395

313 <210> SEQ ID NO: 10

314 <211> LENGTH: 362

315 <212> TYPE: DNA

316 <213> ORGANISM: fusion

318 <400> SEQUENCE: 10

319 gactacaagg atgacgacga caaggccctg gataccaaact actgcttcag ctccacggag 60
321 aagaactgt gcgtcgccca gctctacatt gacttccggc aggacctggg ctggaaagtgg 120
323 attcatgaac ccaaggggctc catgccaatt tctgcctggg gccctgtccc tacatctgg 180
325 gccttagacac tcagtagacgc aaggtcctgg ctctgtacaa ccagcacaaac cgggcgcgt 240
327 cggcggcgcc gtgctgcgtg ccgcaggcgc tggagccact gcccatcggt tactacgtgg 300
329 gccgcaagcc caaggtggag cagctgtcca acatgatcggt gcgttccgtc aagtgcagct 360
331 ga 362

334 <210> SEQ ID NO: 11

335 <211> LENGTH: 120

336 <212> TYPE: PRT

337 <213> ORGANISM: fusionprotein

339 <220> FEATURE:

340 <221> NAME/KEY: PEPTIDE

341 <222> LOCATION: (1)..(8)

342 <223> OTHER INFORMATION: FLAG tag

345 <400> SEQUENCE: 11

347 Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe 15
348 1 5 10 15

351 Ser Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe 30
352 20 25 30

355 Arg Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His 45
356 35 40 45

359 Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr 60
360 50 55 60

363 Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala 80
364 65 70 75

367 Ser Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile 95
368 85 90

371 Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met 110
372 100 105

375 Ile Val Arg Ser Cys Lys Cys Ser 120

376 115

379 <210> SEQ ID NO: 12

380 <211> LENGTH: 1197

381 <212> TYPE: DNA

382 <213> ORGANISM: fusion

384 <220> FEATURE:

385 <221> NAME/KEY: CDS

Please correct this error in
subsequent sequences

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/017,372

DATE: 01/02/2002
TIME: 11:25:33

Input Set : A:\61302.ST25.txt
Output Set: N:\CRF3\01022002\J017372.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date